REMARKS/ARGUMENTS

Amendments to the claims.

Claim 71 is currently amended. Claim 76 is cancelled. New claim 79 is added. After this amendment, claim 71-79 will remain in this application.

No new matter is added by this amendment.

Support for "said polypeptide comprises a first conserved domain that is at least 65% identical to amino acids 134-199 of SEQ ID NO: 4" in claim 71 is found in the paragraph [0081] of US patent application no. 10/675,852, to which the present application claims priority.

A basis for "a second conserved domain that is at least 74% identical to amino 332-401 of SEQ ID NO: 4, and a third conserved domain that is at least 60% identical to amino 405-478 of SEQ ID NO: 4" may be found in Table 1 beginning at the last row of page 35.

Support to the amendment of claim 76 may be found, for example, on page 112 at lines 9-13. Please also see page 147 beginning at line 7: "Table 10 compares the survival ratings of *Arabidopsis* plants overexpressing various polypeptides, evaluated after seven to eight days of drought treatment, rewatering, and two to three days of a recovery period. Values indicate the median odds of survival within a given flat (the 50th percentile of survival within each pot of a given genotype per line divided by the average wild-type survival in the flat)" (the paragraph spanning page 147 and 148). Table 10 shows that transgenic plants transformed with G922 has a higher median odds of survival (1.406) than controls (0.800).

The instant amendments are being made in response to the final Office action, and were not made previously for that reason.

Response to specific items within the Office action.

Item 6 and 8. Rejection under 35 USC 112, second paragraph and first paragraph,

Claim 76 has been amended to avoid this rejection. Please see the basis provided for the amendment in the previous section of this response.

Accordingly, Applicants respectfully request that these rejections be withdrawn.

Item 9. Rejection under 35 USC 112, first paragraph, written description

Applicants respectfully traverse the rejection and its supporting remarks. However, in order to facilitate prosecution in this case Applicants have amended the pending claims, without prejudice or disclaimer. Claim 71 has been amended to include more structural limitation to direct to transgenic plants comprising a recombinant polynucleotide encoding a polypeptide that is at least 60% identical to SEQ ID NO: 4 and three specific conserved domains. Accordingly, one of skill in the art would clearly understand that Applicants had possession of the claimed invention.

Applicants have provided the polypeptide sequences G922, SEQ ID NO: 4, G3810, SEQ ID NO: 212, and G3811, SEQ ID NO: 214. Applicants note that there are several disclosed and art-recognized alignment methods to compare two sequences. The specification has taught that "[g]roups of similar genes can also be identified with pair-wise BLAST analysis" (page 52, lines 17-19). The BLAST analysis has demonstrated that G3810 and G3811 are 65% and 61% identical to G922, SEQ ID NO: 4, respectively (please see attached Exhibit A). An analysis by an Accelrys based method submitted with the response to a previous office action also indicates that G3810 and G3811 are 65.9% and 62.8% identical to that of G922. The allegation in the Office action that "G3811 is only 57.2% identical to SEQ ID NO: 4. [t]hus G3811 falls outside of the claimed genus" appears to have no support and all three disclosed variants G922, G3810 and G3811 share a sequence identity of at least 60% with SEQ ID NO:4. G922 has been shown to confer enhanced water deprivation tolerance when overexpressed in a plant (page 119, lines 1-3) and G3810 and G3811 also have similar function as shown in previously submitted declaration by Dr. Ratcliffe. Applicants have provided in Table 1 the identifying structural elements: the three conserved SCR domains that are homologous to that of SEQ ID NO: 4 through sequence alignment as shown in Figure 19A-19R. Applicants have also described a fourth "ser/pro-rich domain that is unique to the G922 clade" on page 10, lines 11-12 and in Fig. 19N Since these functional sequences possess the described structural elements and are derived from diverse plant species such as soy and *Arabidopsis*, they represent a statistical sampling of a large number of plant sequence species encompassed by the claimed genus. Applicants believe that the extent of the instant disclosure in support of the claimed invention is at least commensurate with that of Example 11 in USPTO's the written description guidelines (Revision 1, March 25, 2008) where the disclosure of just two conserved domains and one singular species of the claimed genus is deemed to have met the written description requirement. Therefore, Applicants believe that the instant disclosure of three conserved structural elements that are common to the claimed genus of sequences, and at least three representative functional species that have the sequence identity of at least 60% to SEQ ID NO: 4, adequately supports the claimed invention.

The Office action stated that Applicants appear to only describe one species that confers water deprivation tolerance to a transgenic plant that fall into the claims of 80% or 95% identical to SEQ ID NO: 4. Applicants respectfully disagree with this assessment. As described above, Applicants have provided three representative variants: G3811, G3810 and G922, which have the sequence identity of 61%, 65% and 100% to SEQ ID NO: 4, and have the function of conferring greater water deprivation tolerance to transgenic plants when overexpressed relative to controls. G3811 and G3810 are the only orthologs of G922 have been tested to date. Applicants have also disclosed the conserved structural elements, i.e. the three conserved SCR domains corresponding to amino acids 134-199, 332-401 and 405-478 of SEQ ID NO: 4, that are always present in the sequences that have functioned by conferring water deprivation tolerance. One of ordinary skill in the art would recognize that sequences having higher similarity in structure, i.e. higher than 65% to SEQ ID NO: 4 would more likely have similar functions to that of SEQ ID NO: 4 than would G3810 or G3811. Sequences with higher homology, for example, 80% or 95% or even greater sequence identity to SEQ ID NO: 4, could be readily made through conserved amino acid substitutions or similar amino acid substitutions, for example, the substitutions listed in Table 3 or Table 4 of the specification, outside the conserved SCR domains, and they would have the similar function to G922. These disclosed polypeptide sequences having the described structure and function are derived from very diverse species, including soy and *Arabidopsis* and they represent a considerably large number of plant sequence species. It is noted that Applicants are not required to exemplify each and every claimed embodiment of his or her invention. Rather, "if a person of ordinary skill in the art would have understood the inventor to have been in possession of the claimed invention at the time of filing, even if every nuance of the claims is not explicitly described in the specification, then adequate written description requirement is met" (*In re Alton*, 37 USPQ2d 1578, 1584 (Fed. Cir. 1996)). Thus one of ordinary skill in the art would recognize that at the filing time, Applicants were in possession of the sequences that and encode the polypeptides having at least 60% amino acid sequence identity to SEQ ID NO:4.

Accordingly, Applicants respectfully request that the rejection under 35 U.S.C. §112, first paragraph, for lack of written description, be withdrawn.

Item 10. Rejection under 35 USC 112, first paragraph, enablement

Applicants respectfully traverse this rejection for the reasons set forth below.

The specification provides a genus of sequences that are homologous to the listed sequences and share three distinct conserved SCR domains, disclosed in Table 1 beginning on page 34. The fully tested G922 transcription factor family members: G922 (SEQ ID NO: 4), G3810 (SEQ ID NO: 212) and G3811

(SEQ ID NO214), conferred enhanced water deprivation tolerance when overexpressed in transgenic plants. These sequences are derived from diverse plant species, such as *Arabidopsis* and soy and they represent a practical sampling of a large number of sequence species. It seems unlikely that, among over 170,000 eudicot plants, *Arabidopsis*, the model plant being studied because of its small size, short life cycle, obligate autogamy and high fertility, and soy, the first crop species being examined, are the only plant species that have sequences that are structurally and functionally related to SEQ ID NO: 4. One of ordinary skill in the art would recognize that a large number of sequences encompassed by the claims can be readily found in species that lie in the intermediate position in the evolutionary tree. Applicants have disclosed how to isolate the sequence by percent identity and similar amino acid substitution or conservative amino acid substitution.

The Office action stated that "applicants only teach how to make and use transcription factors to impart greater tolerance to water deprivation, yet the instant claims are not so limited." In response, Applicants have disclosed that the polypeptides in the claimed invention are not limited to the transcription factors or peptides that can regulate transcription. For example, page 24, lines 3-7 of the specification stated "The sequences of the present invention may be from any species, particularly plant species, in a naturally occurring form or from any source whether natural, synthetic, semi-synthetic or recombinant" and page 26, lines 1-4 stated that "[t]he present invention provides… novel sequence variant polypeptides or polynucleotides encoding novel variants of transcription factors derived from the specific sequences provided here". Since Applicants have provided the closely correlated structural elements among the claimed genus of polypeptides, i.e. having a sequence identity of at least 60% to SEQ ID NO: 4 and having a conserved domain of at least 65% identical to amino acids 134-199 of SEQ ID NO: 4, and the function of conferring improved water deprivation tolerance, it is not relevant whether the polypeptide is a true transcription factor or not. For example, one of ordinary skill in the art could readily make polynucleotide sequence variants encoding polypeptides that have the structure and function based on conservative amino acid substitutions and transform the polynucleotide sequences into plants without having to pre-determine whether the encoded polypeptides are transcription factors or not.

Given the disclosure of the conserved structure elements and related functional characteristics present in examplar sequences from diverse plant species, the detailed guidance of how to identify sequences of the disclosed structure and function through percent identity, and the knowledge in the art at the time of filing, it would at most require routine experimentation to obtain other sequences encoding polypeptides having more than 60% sequence identity to SEQ ID NO: 4 and conferring enhanced water

deprivation tolerance when overexpressed. Thus, Applicants believe that the full scope of currently claimed subject matter is enabled.

Accordingly, Applicant respectfully requests that the rejection of the claims under 35 USC 112, first paragraph, for lack of enablement, be withdrawn.

Item 11. Rejection under 35 USC 103 (a)

The Examiner repeats the rejection under 35 USC (a) based on the teachings of Benfey et al (WO97/41153). This rejection has been in part avoided by the amendments and in part respectfully traversed for the reason set forth below.

The claims have been amended and are instantly directed to transgenic plants comprising polynucleotides that encode polypeptides that are at least 60% identical to SEQ ID NO: 4 and have three conserved domains that are highly homologous to those of SEQ ID NO: 4. Applicants have the disclosed that the claimed genus of polypeptides contains the distinct SCR domains, the presence of which correlate with the claimed functions. G3810, G3811 and G922 have conserved 1st SCR domains that are at 68%, 74% and 100% to that of SEQ ID NO: 4. In contrast, Benfey's sequence lacks a significant portion of the protein (157 amino acid residues) and contains only 63% (42 amino acid residues out of 66 amino acid residues) of the 1st SCR domain of SEQ ID NO: 4. The sequences provided below include G922 (SEQ ID NO: 4 of the instant application) and the Benfey sequence SRPa3 (SEQ ID NO: 21 of the Benfey application WO97/41153):

G922, SEQ ID NO:4 of the instant application (482 amino acids) the 1st SCR domain is underlined.

MVAMFQEDNGTSSVASSPLQVFSTMSLNRPTLLASSSPFHCLKDLKPEERGLYLIHLLLTCANHV
ASGSLQNANAALEQLSHLASPDGDTMQRIAAYFTEALANRILKSWPGLYKALNATQTRTNNVSE
EIHVRRLFFEMFPILKVSYLLTNRAILEAMEGEKMVHVIDLDASEPAQWLALLQAFNSRPEGPPH
LRITGVHHQKEVLEQMAHRLIEEAEKLDIPFQFNPVVSRLDCLNVEQLRVKTGEALAVSSVLQLH
TFLASDDDLMRKNCALRFQNNPSGVDLQRVLMMSHGSAAEARENDMSNNNGYSPSGDSASSLP
LPSSGRTDSFLNAIWGLSPKVMVVTEQDSDHNGSTLMERLLESLYTYAALFDCLETKVPRTSQDR
IKVEKMLFGEEIKNIISCEGFERRERHEKLEKWSQRIDLAGFGNVPLSYYAMLQARRLLQGCGFD
GYRIKEESGCAVICWQDRPLYSVSAWRCRK

SRPa3, SEQ ID NO: 21 of the Benfey application (325 amino acids) the 1st SCR domain is underlined.

AMEGEKMVHVIDLDASEPAQWLALLQAFNSRPEGPPHLRITGVHHQKEVLEQMAHRLIEEAEKL
DIPFQFNPVVSRLDCLNVEQLRVKTGEALAVSSVLQLHTFLASDDDLMRKNCALRFQNNPSGVD
LQRVLMMSHGSAAEARENDMSNNNGYSPSGDSASSLPLPSSGRTDSFLNAIWGLSPKVMVVTEQ
DSDHNGSTLMERLLESLYTYAALFDCLETKVPRTSQDRIKVEKMLFGEEIKNIISCEGFERRERHE
KLEKWSQRIDLAGFGNVPLSYYAMLQARRLLQGCGFDGYRIKEESGCAVICWXDRPLYSVSAW
RCRK

Benfey deduces a large number of sequences by comparing the *Arabidopsis* SCR, SEQ ID NO: 2 in WO97/41153, with sequences in available databases (Table 1 of WO97/41153) and discloses the genus of the sequences as containing one or multiple motifs of the six conserved motifs (page 8, lines 24-30 of the Benfey publication WO9741152), these motifs are very different from the conserved SCR domains in the instant disclosure. It is noted that in order to determine obviousness or nonobviousness, both the claimed invention and the prior art must each be viewed as a whole. In *in re Langer*, 465 F.2d 896, 175 USPQ 169 (CCPA 1972), the claims to a polymerization process using a sterically hindered amine were held unobvious over a similar prior art process because the prior art disclosed a large number of unhindered amines and only one sterically hindered amine (which differed from a claimed amine by 3 carbon atoms), and therefore the reference as a whole did not apprise the ordinary artisan of the significance of hindered amines as a class. Similarly, Benfey discloses a large number of sequences that lack the conserved structural elements and the claimed function, and only one species, i.e., SRPa3, whose function was yet to be confirmed, which resembles a portion of one claimed species of the instant invention, i.e.SEQ ID NO: 4. Therefore, Benfey's disclosure as a whole does not apprise the ordinary artisan of the significance of the claimed genus.

In addition, the Benfey reference does not provide an enabling disclosure regarding SRPa3, SEQ ID NO: 21. Although Benfey suggests that SCR may confer thicker roots ("plants engineered with SCR overexpression ***may*** exhibit improved vigorous growth characteristics when cultivated under conditions where large and thicker roots are advantageous", page 154 at line 11, ***emphasis*** added), he does not provide evidence as to the function of SEQ ID NO: 21. It is noted that a conclusion of obviousness requires that the reference(s) relied upon be enabling in that it put the public in possession of the claimed invention (see, *In re Hoeksema*, 399 F.2d 269, 274, 158 USPQ 596, 601 (CCPA 1968)). Benfey's broadly-drawn claim 18 of Benfey's publication "A plant engineered to overexpress the SCARECROW protein, so that cell division is increased in roots, resulting in thicker root development." is not enabled for plants overexpressing SRPa3, SEQ ID NO: 21 since Benfey never transformed a plant with the polynucleotide encoding SRPa3, SEQ ID NO: 21 and tested its function. Without the results from rigorous experimental testing, one ordinary skill in the art would not recognize if there is a useful function associated with this sequence at all, which does not even encode a full-length protein. Without an enabling disclosure, one of ordinary skill in the art would not be motivated to isolate the complete coding sequence and to make transgenic plants that overexpress SRPa3, SEQ ID NO: 21.

The statement in the Office action "it would have been obvious to isolate a complete coding region [based on the partial sequence] and transform a plant …" is to allege that the possession of the

partial sequence (SEQ ID NO: 21 of the Benfey application) also places Benfey in possession of the much longer full-length sequence (the instant SEQ ID NO: 4). This assertion is inconsistent with case law teachings regarding what is required to effect possession of DNA structures. Applicants note that in *In re Deuel*, 35 U.S.P.Q.2d 1210 (Fed. Cir. 1995), the Federal Circuit held that claims directed to polynucleotides that encode a particular polypeptide should not be considered obvious in view of a prior art reference that taught methods of cloning, when combined with a reference that taught a partial amino acid sequence of the polypeptide. The Federal Circuit stated that because the claims at issue were directed to a specific chemical structure (i.e. a nucleotide sequence), a *prima facie* case of obviousness should be based on teachings in the prior art that suggest the particular structure being claimed, irrespective of whether the methods used to arrive at the particular chemical structure were obvious. The Federal Circuit noted that, "[n]ormally a prima facie case of obviousness is based upon structural similarity, i.e., an established structural relationship between a prior art compound and the claimed compound." In the absence of such structural similarity in the prior art, the court held that a rejection based on obviousness is not proper. Furthermore, the court in *Deuel* noted that the "…PTO's focus on known methods for potentially isolating the claimed DNA molecules is also misplaced because the claims at issue define compounds, not methods…. [T]he issue is the obviousness of the claimed compositions, not of the method by which they are made." Accordingly, the Federal Circuit was clear in *Deuel* that "…the existence of a general method of isolating cDNA or DNA molecules is essentially irrelevant to the question whether the specific molecules themselves would have been obvious…"

By stating "it would have been obvious to isolate a complete coding region…" the Office action seems to argue that the method for isolating the complete sequence based on a partial sequence is available to one skilled in the art. However, the controlling issue here is not whether the isolating the complete sequence is enabled by means of one of ordinary skill in the art, but whether Benfey envisioned/suggested the complete DNA sequence or not. *Fiers v. Sugano* and *University of California v Eli Lilly* established that possession of a DNA structure must be defined by its sequence or other physical properties. This case law affirms that possession is neither defined by functionality alone nor by the availability of art-recognized means to prepare or obtain the DNA structure. By analogy to chemical practice where one skilled in the art can distinguish or envisage numerous species encompassed within a generic formula, the characteristic of the 157 additional amino acids present in the complete sequence (instant SEQ ID NO: 4) must be envisaged from the structure of SEQ ID NO: 21 within generic claim 18 of Benfey application. No rational basis exists to support such an event and, therefore, no rational basis exists to support the Benfey suggests or teaches the full-length structure. The illogical conclusion that a

prior disclosure of the partial sequence SEQ ID NO: 21 would render the full length sequence obvious is further debunked by case law teachings of *In re Bell*, 991 F.2d 781, 26 USPQ2d 1529 (Fed. Cir. 1993), where the Federal Circuit reversed the Board's decision that Bell's claim of a nucleotide sequence is obvious over the combined teachings of the amino acid sequence encoded by the nucleotide and the method for isolating a gene for which at least a short amino acid sequence of the encoded protein is known, because "Bell claims compositions, and the issue is the obviousness of the claimed compositions, not of the method by which they are made."

In *Fiers v. Sugano* (984 F2d 1164, 25 U.S.P.Q. 2d 1601 (Fed. Cir. 1993)), an early disclosure that lack "an intact complete gene", analogous to Benfey's disclosure on SRPa3, was deemed insufficient to support a claim on the complete gene in the later-filed application. The court reiterated "[a]n adequate written description of a DNA requires more than a mere statement that it is part of the invention and a reference to a potential method for isolating it; what is required is a description of the DNA itself." Benfey's application does not describe the complete coding sequence itself, nor does it disclose a method actually leads to the DNA. It would require undue trial and error experimentation involving multiple steps, for example, RNA isolation, reverse transcription, PCR amplification, to obtain the full length cDNA sequence from the mere description of the partial sequence contained in an EST clone. Benfey did not teach which method one could use to generate the complete sequence. Even if he did, the court teaches "A bare reference to a partial DNA with a statement that it can be obtained by reverse transcription is not a description (which Benfey does not even disclose); does not indicate … [the] possession of the complete DNA sequence" (*supra*). The CAFC rejected the argument that "the existence of a workable method for preparing a DNA establishes conception of that material" and stated "[o]ur statement in Amgen that conception may occur, *inter alia*, when one is able to define a chemical by its method of preparation requires that the DNA be claimed by its method of preparation." In the present case, Benfey claims the sequence itself (SEQ ID NO: 21), not by its method of preparation. The CAFC stated "conception of a substance claimed *per se* without reference to a process requires conception of its structure, name, formula, or definitive chemical or physical properties." The product, such as the complete sequence (SEQ ID NO: 4 of the instant application) is not conceived in the prior art reference until one can define it other than by its biological activity or function. With an only a partial sequence that lacks one third of the coding sequence, and an important structural domain, Benfey fails to define or suggest the complete sequence by this standard. Therefore, Benfey's disclosure is inadequate to put the public in possession of the invention of SEQ ID NO: 4 and thus does not render the present invention obvious.

Furthermore, Benfey did not transform the SRPa3 sequence into plants, nor does it provide functional data regarding the SRPa3, SEQ ID NO:21 transgenic plants, Applicants note that Benfey's disclosure fails to teach water deprivation tolerance either expressly or implicitly. Regarding "[i]t would have been obvious to one of ordinary skill in the art that thicker root development would confer greater tolerance to water deprivation", Applicants respectfully disagree. As one of ordinary skill in the art knows, a plant's ability to tolerate water deprivation depends on mechanisms that maintain cell water content such as osmotic regulation and stromatal closure, and is determined by multiple factors, for example, adaptations of the stomata to reduce water loss, such as reduced numbers or waxy surfaces, water storage in succulent above-ground parts or water-filled tubers, adaptations in the root system to increase water absorption, trichomes (small hairs) on the leaves to absorb atmospheric water (from: en.wikipedia.org/wiki/Drought_tolerance). Thus, thicker root development alone would not necessarily account for water deprivation tolerance. In Applicants' own studies, out of the twenty lines of plants transformed with SEQ ID NO: 3 encoding the full length protein that corresponds to Benfey's partial sequence exhibited water deprivation tolerance, eighteen lines' root development is undistinguishable from the controls, and the rest two lines showed less root development than in control plants (please see the declaration by Dr. Reuber as attached). This result confirmed that conferring greater tolerance to water deprivation is not obvious merely from the function of conferring thicker root development. This study casts doubt on Benfey's asertion that SCARECROW proteins, which include SEQ ID NO: 21and the corresponding full-length protein, may confer thicker roots in transgenic plants relative to controls even if the complete sequence were obtainable. Based on Benfey's teaching, plants that showed greater tolerance to water deprivation from Applicant's experiments would have been missed by one of ordinary skill in the art since they did not possess thicker roots relative to controls. Therefore, Benfey's disclosure of SEQ ID NO: 21 does not render the instant claims pertaining to SEQ ID NO: 4 obvious.

Accordingly, Applicants respectfully request the rejection under 103 (a), be withdrawn.

CONCLUSION

Applicants believe that no additional fee is due with this communication. However, if the USPTO determines that an additional fee is due, the Commissioner is hereby authorized to charge Mendel Biotechnology, Inc. Deposit Account No. 50-1025.

Respectfully submitted,
MENDEL BIOTECHNOLOGY, INC.

Date: August 24, 2009

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Attachment: declaration_TLR

Exhibit A. Comparison of G922 and phylogenetically related sequences

BLAST results with G922, SEQ ID NO: 4.

G3810 (Amino Acid Sequence)

Identities = 291/444 (65%)

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G922:     KDLKPEERGLYLIHLLLTCANHVASGSLQNANAALEQLSHLASPDGDTMQRIAAYFTEAL
          +++K EERGLYLIHLLL+CANHVA+G+L+NAN  LEQ+S LASPDGDTMQRIA YF E+L
G3810:    REMKSEERGLYLIHLLLSCANHVAAGNLENANTTLEQISMLASPDGDTMQRIATYFMESL

G922:     ANRILKSWPGLYKALNATQTRTNNVSEEIHVRRLFFEMFPILKVSYLLTNRAILEAMEGE
          A+RILK+WPG+++ALN+T+     +S+EI V++LFFE+FP LKV+++LTN+AI+EAMEGE
G3810:    ADRILKTWPGIHRALNSTKMTL--ISDEILVQKLFFELFPFLKVAFVLTNQAIIEAMEGE

G922:     KMVHVIDLDASEPAQWLALLQAFNSRPEGPPHLRITGVHHQKEVLEQMAHRLIEEAEKLD
          K++H+IDL+A+E AQW+ALL+  ++ PEGPPHLRITGVH +KE+L+++AHRL EEAEKL
G3810:    KVIHIIDLNAAEAAQWIALLRVLSAHPEGPPHLRITGVHQKKEILDEVAHRLTEEAEKLD

G922:     IPFQFNPVVSRLDCLNVEQLRVKTGEALAVSSVLQLHTFLASDDDLMRKNCALRFQNNPS
          IPFQFNPV S+L+ L+ ++LRVKTGEALA+SS+LQLHT LA DD+ M++   L  +++ +
G3810:    IPFQFNPVASKLENLDFDKLRVKTGEALAISSILQLHTLLAWDDEAMQRKSPLLLKSS-N

G922:     GVDLQRVLMMSHGSAAEARENDMSNNNGYSPSGDSASSLP----LPSSGRTDSFLNAIWG
          G+ LQRVL M   +  +  E DM N  GY+PS DS SS P      +S   +SFLNA+WG
G3810:    GIHLQRVLPMGQSTLGDLLEKDMVN--GYTPSPDSTSSSPSSLTTSNSMNMESFLNALWG

G922:     LSPKVMVVTEQDSDHNGSTLMERLLESLYTYAALFDCLETKVPRTSQDRIKVEKMLFGEE
          LSPKVMVVTEQD +HNG TLM+RLLE+LY+YAALFDCLE+ V RTS +R++VEKMLFGEE
G3810:    LSPKVMVVTEQDCNHNGPTLMDRLLEALYSYAALFDCLESTVSRTSLERLRVEKMLFGEE

G922:     IKNIISCEGFERRERHEKLEKWSQRIDLAGFGNVPLSYYAMLQARRLLQGCGFDGYRIKE
          IKNII+CEG ER+ERHEKLEKW QR DLAGFGNVPLSY+ M+QARR LQ  G +GYR+++
G3810:    IKNIIACEGSERKERHEKLEKWFQRFDLAGFGNVPLSYFGMVQARRFLQSYGCEGYRMRD

G922:     ESGCAVICWQDRPLYSVSAWRCRK
          E+GC +ICW+DRP+YS+SAWR RK
G3810:    ENGCVLICWEDRPMYSISAWRSRK
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G3811 (Amino Acid Sequence)

Identities = 276/449 (61%)

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G922:     SPFHCLKDLKPEERGLYLIHLLLTCANHVASGSLQNANAALEQLSHLASPDGDTMQRIAA
          SP+H    +K E RGL LIHLLL  AN VA+G LQ A   LEQ+S  AS DGDTMQRIA+
G3811:    SPYH----MKCELRGLVLIHLLLAGANFVATGDLQYAYLTLEQISQHASLDGDTMQRIAS
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G922:     YFTEALANRILKSWPGLYKALNATQTRTNNVSEEIHVRRLFFEMFPILKVSYLLTNRAIL
          Y +EALA+RILK+WPG+++ALN++  R   VS+EI V++LFFE+ P LK SY+LTN+AI+
G3811:    YVSEALADRILKTWPGIHRALNSS--RITMVSDEILVQKLFFELLPFLKFSYILTNQAIV

G922:     EAMEGEKMVHVIDLDASEPAQWLALLQAFNSRPEGPPHLRITGVHHQKEVLEQMAHRLIE
          EAMEGEKMVH++DL  + PAQW++LLQ  ++RPEGPPHLRITGVHH+KEVL+QMAH+L E
G3811:    EAMEGEKMVHIVDLYGAGPAQWISLLQVLSARPEGPPHLRITGVHHKKEVLDQMAHKLTE

G922:     EAEKLDIPFQFNPVVSRLDCLNVEQLRVKTGEALAVSSVLQLHTFLASDDDLMRKNCALR
          EAEKLDIPFQFNPV+S+L+ L+  +LRVKTGEALA+SS++QLH+ LA D+D  R+   L
G3811:    EAEKLDIPFQFNPVLSKLENLDFNKLRVKTGEALAISSIMQLHSLLALDEDASRRKSPL-

G922:     FQNNPSGVDLQRVLMMSHGSAAEARENDMSNNNGYSPSGDSASSLPLPSSG---RTDSFL
             N + + LQ+ L+M+H +  +  +       GYSPS DSASS P  SS     ++SFL
G3811:    LSKNSNAIHLQKGLLMNHNTLGDLLD-------GYSPSPDSASSSPAASSSALMNSESFL

G922:     NAIWGLSPKVMVVTEQDSDHNGSTLMERLLESLYTYAALFDCLETKVPRTSQDRIKVEKM
          NA+WGLSPKVMVVTEQD +HN  T+MERL E+L++YAA FDCLE+ V R S DR+K+EKM
G3811:    NALWGLSPKVMVVTEQDFNHNCLTMMERLAEALFSYAAYFDCLESTVSRASMDRLKLEKM

G922:     LFGEEIKNIISCEGFERRERHEKLEKWSQRIDLAGFGNVPLSYYAMLQARRLLQGCGFDG
          LFGEEIKNII+CEG ER+ERHEK+++W QR+DL+GF NVP+SYY MLQ RR LQ  G +G
G3811:    LFGEEIKNIIACEGCERKERHEKMDRWIQRLDLSGFANVPISYYGMLQGRRFLQTYGCEG

G922:     YRIKEESGCAVICWQDRPLYSVSAWRCRK
          Y+++EE G  +ICWQ+R L+S++AWR RK
G3811:    YKMREECGRVMICWQERSLFSITAWRPRK
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